Bal DE	89.3	70.2	58.2	51.1	49.1	41.4	40.5	36.5	35.5	33.4	33	29.6	29.6	28.8	28.8	25.2	24.6	24.4	23.9	23.2	22.1	21.1	21.1	20.1	20.1	6.61	19.5	19.4	17.8	7.71	17.7	17.5	17.1	17.1	16.3
Annotation	phosphomevalonate kinase [Homo sapiens]	fibronectin [Danio reno]	Human MHC Class I HLA heavy chain (HLA-B-7301) mRNA, complete cds.	alpha2(I) collagen [Homo sapiens]			connective tissue growth factor [Homo sapiens]		Gig I protein [Homo sapiens]	prostacyclin-stimulating factor (PSF) [Homo sapeins]	carbonic anhydrase VII [Homo sapiens]	SM22 alpha [Homo sapiens]	dJ977B1.5 (myosin regulatory light chain 2, smooth muscle isoform) [Homo sapiens]	lectin precursor [Homo sapiens]	complement component C1s [Homo sapiens]	1-8U [Homo sapiens]	thrombospondin [Mus musculus]	insulm-like growth factor binding protein 3 [Homo sapiens]	p21/WAF1 [Felis catus]	follistatin-related protein precursor [Homo sapiens]	quiescin [Homo sapiens]	putative p33 [Homo sapiens]	precursor of C1r (AA -17 to 688) [Homo sapiens]	integral membrane serine protease Seprase [Homo sapiens]	thrombospondin 2 [Bos taurus]	extracellular protein [Homo sapiens]	protein with miniactivin activity [synthetic construct]	transforming growth factor induced protein [Oryctolagus cuniculus]	Dickkopf-3 [Homo sapiens]	I-caldesmon II [Homo sapiens]	_	_		•	fibrilin-! [Mus musculus]
E-value	1.00E-107	0	3.00E-35	0	0	0	0	1.00E-145	0	0	1.00E-160	1.00E-114	1.00E-86	8.00E-77	0	3.00E-64	0	1.00E-145	1.00E-22	1.00E-166	0	1.00E-121	0	0	0	5.00E-75	0	0	3.00E-41	6.00E-96	9.00E-96	0	8.00E-79	0	0
GenBank Hit E-value	g1294782	g3420846	g439858	g2388555	g818	g386997	g180924	g34388	g2181871	g861521	g179967	g2340833	g6983729	g307122	g179646	g23398	g511869	g398164	g2588789	g536898	g3004502	g32131	g29539	g1924982	g2995138	g458228	g512778	g1518107	g6070253	g219898	g180194	g5815461	g3273405	g3168993	g726324
Clone ID	1497123	3553729	2859033	1870965	1672744	1445767	1674454	079576	1514989	690313	2329216	4049957	1572533	2495131	1904751	2949427	2055534	1447903	1804548	1987358	1854220	1001730	1664320	2483605	2804667	1798209	557012	2056395	3142736	1319608	1319608	1958902	1851696	1851696	1448051
Template ID	1497123CB1	2985802CB1	475532.4	3138290CB1	474310.40	410580.16	337518.25	1303785CB1	1044033.4	1000222.31	403873.4	1383105.12	1383354.13	697785CB1	420115CB1	1101453.2	1399366.20	3072333CB1	1270681.1	1505038CB1	1035602.5	1330167.3	1003386CB1	1097334.1	959142CB1	1359783CB1	063646CB1	1519595CB1	2054176CB1	1312325CB1	022404.25	1787335CB1	1193648.7	1193648.1	1867861CB1
SEQ ID NO	-	2	m	4	5	9	7	∞	6	10	Ξ	12	13	14	15	91	11	18	61	20	21	22	23	24	25	56	27	28	56	30	31	32	33	34	35

Bal DE	16.3	16.2	15.5	15.3	15.2	14.9	14.7	14.5	13.8	13.7	13.6	13.5	13.5	13.1	12.8	12.3	12.1	12	6.11	6:11	11.8	11.8	11.5	11.5	11.2	10.9	10.9	8.01	9:01	10.4	10.4	10.3	10.3	10.2	
Annotation	down syndrome candidate region 1; one of four alternatively spliced exon 1 [Homo sapiens]	interferon-inducible protein [Homo sapiens]	prion protein (p27-30) [Homo sapiens]	moesin B [Homo sapiens]	deleted in liver cancer-1 [Homo sapiens]	transforming growth factor-beta 1 binding protein precursor [Homo sapiens]	lysyl oxidase [Homo sapiens]	collagen alpha3(VI) [Mus musculus]	myosin regulatory light chain [Homo sapiens]	pro-alpha 1 (11) collagen (313 AA; AA 975-271c) [Homo sapiens]	tumor necrosis factor [Homo sapiens]	alpha-tropomyosin 5b [Rattus norvegicus]	hypothetical protein [Homo sapiens]	prepro-alpha1(I) collagen [Homo sapiens]	guanylate binding protein isoform I [Mus musculus]	ferntın light chain [Homo sapiens]	alpha 1(VIII) collagen [Homo sapiens]	dJ65P5.1 (reticulocalbin 1, EF-hand calcium binding domain) [Homo sapiens]	microsomal glutathione transferase [Homo sapiens]	glutathione S-transferase [Homo sapiens]	carbonate dehydratase [Homo sapiens]	Human mRNA for integrin beta 1 subunit.	type IV collagenase [Mus musculus]	erythroid differentiation protein precursor [Homo sapiens]		Irp [Homo sapiens]		aspartyl (asparaginyl) beta hydroxylase [Bos taurus]	cysteine-rich protein [Homo sapiens]	unknown (Homo sapiens)	-	collagen type IV alpha 5 chain [Homo sapiens]	_		Interierun-gamma muccu piotem [momo sapiems]
t E-value	2.00E-94	4.00E-67	8.00E-81	0	0	0	0	0	1.00E-84	1.00E-152	0	2.00E-95	6.00E-83	1.00E-154	0	2.00E-90	1.00E-89	0	1.00E-73	3.00E-78	0	0	0	0	6.00E-35	0	1.00E-153	0	2.00E-89	1.00E-146	1.00E-143	1.00E-165	1.00E-132	1.00E-119	>
GenBank Hit E-value	g2612868	g1177476	g6996155	g188626	g2654198	g339548	g187189	g4104232	g34756	g30097	g339992	g207508	g4884393	g1418928	g193440	g182514	g30082	g5748581	g1195483	g306808	g693933	g31441	g198466	g181947	g507252	g895840	g31438	g162694	g181071	g704441	g38416	g180825	g2822169	g8176525	8184007
Clone ID	1650238	2902903	1720056	1733490	3084122	1313183	1852047	1314882	078783	2518178	1700071	1572555	1572555	782235	521139	2868138	3118643	2057296	1995380	1995380	1319020	417451	1558081	2242648	027775	1394401	1720114	3693273	2852042	1402715	1618422	2606307	459651	2508261	7208701
Template ID	5511889CB1	3094768CB1	1256895CB1	2019981CB1	2708240CB1	1092427.1	351841.7	022221.43	2190217CB1	410910.3	1966280CB1	430669.39	430669.23	1870753CB1	3173735CB1	1330185.14	2314132CB1	2508205CB1	3326672CB1	234202.34	078242CB1	220943.20	1383320.13	3526170CB1	184081.24	1821331CB1	3660006CB1	089172.13	3084563CB1	241227.17	348151.2	1720808CB1	998552.6	040652.35	040052.36
SEQ ID	36	37	38	39	9	41	42	43	4	45	46	47	48	49	20	51	52	53	\$	55	99	57	28	59	99	61	62	63	2	65	99	<i>L</i> 9	89	69 6	?

-	bal DE	10.1	6.6	9.6	9.6	9.5	9.4	9.4	9.3	9.3	9.3	9.2	9.2	9.2	9.1	9.1	9.1	9.1	6	6	8.9	8.9	8.8	8. 8.	80 80 80	8.7	8.7	8.5	8.5	8.5	8.4	8.4	8.4	8.3	 	%; ?:
			s cell surface protein [Homo sapiens]) ecto-5'-nucleotidase [Mus musculus]	cell surface glycoprotein [Homo sapiens]	3 HDCMA39P [Homo sapiens]) deconn variant A [Homo sapiens]) HLA-DRB1 [Homo sapiens]	3 myosin light chain kinase isoform 2 [Homo sapiens]	5 myosin light chain kınase [Homo sapıens]	asma gene product [Gallus gallus]) laminin gamma 1 precursor [Anopheles gambiae]	laminin B2 chain [Homo sapiens]) XRP2 protein [Homo sapiens]) antigen CD36 [Homo sapiens]) antigen CD36 [Homo sapiens]	aminopeptidase N, APN (type II membrane protein) {EC 3.4.11.2} [Oryctolagus cunculus]) CG6778 gene product [Drosophila melanogaster]	class II antigen [Homo sapiens]) alpha-1 type IV collagen [Homo sapiens]) branching enzyme 1 [Phaseolus vulgarıs]	CG1275 gene product [Drosophila melanogaster]) rhoC coding region (AA 1-193) [Homo sapiens]) Human XIST, coding sequence 'a' mRNA (locus DXS399E).) T-plastin [Rattus norvegicus]) sushi-repeat-contaming protein [Mus musculus]) FLT4 Igand DHM [Homo sapiens]	depetityl peptidase I [Canis familians]) filamın [Homo sapiens]) heat shock protein hsp40 homolog [Homo sapiens]) H-cacherin [Homo sapiens]) endoglin [Homo sapiens]	_) ST4 oncofetal trophoblast glycoprotein [Homo sapiens]
-	Bank Hit E-value	0	4.00E-78	0	1.00E-134	8.00E-58	0	1.00E-120	1.00E-138	5.00E-86	3.00E-37	0	4.00E-99	0	0	0	0	0	5.00E-66	1.00E-143	0	0	0	5.00E-44	1.00E-110	0	0	0	0	0	0	0	0	0	0	O
	Genbank H	g899300	g487809	g3046875	g188256	g7634779	g5532411	g307269	g7239698	g7239696	g211205	g6706335	g186964	g3550283	g180117	g180111	g544755	g7294319	g673417	g5478222	g1805270	g180803	g5441246	g7292213	g36034	g37987	g57381	g6475031	g1373427	g4106126	g1203969	g6031212	g1381792	g3201589	g3201589	g3805947
į	Clone ID	522294	1668794	1718651	162769	3134070	3820761	2105963	1720149	1720149	2102320	1599344	1599344	2057260	3506985	3506985	2771046	2057601	1994472	2683564	2633207	2173208	1867652	1909488	2733928	1514318	1402228	1636171	550425	1822716	1708528	2844989	1404153	3511216	3511216	1283532
-	l emplate ID	082155CB1	190144CB1	234537.3	1088425.1	254547.1	2676170CB1	1092181 1	471362.33	471362.27	1162416.1	252151.12	252151.7	358892.1	1296867CB1	337518.7	1344279CB1	2731776CB1	1090035.1	1089929.9	2723092CB1	2174489CB1	1253978CB1	2274011CB1	3119737CB1	1384695.102	257332CB1	2972880CB1	550425CB1	014284CB1	1091854.7	138709.5	375954.1	1262781CB1	282761.16	3090708CB1
SEQ ID	Q	71	72	73	74	75	76	77	78	79	8	81	82	83	8	82	98	87	88	86	06	91	35	93	25	95	96	26	86	66	100	101	102	103	104	105

	Bal DE	8.2	 	8.1	∞	∞	∞	∞	7.8	7.7	7.7	7.7	7.6	7.6	7.6	7.6	7.5	7.5	7.5	7.4	7.4	7.4	7.2	7.1	7.1	7.1	7	7	7	6.9	6.9	6.9	6.9	6.9	6.7 6.7	
1 777 (11)	Annotation	21 kd basic fibroblast growth factor (ctg start codon; put.); putative [Homo sapiens]	MHC class I chain-related protein A [Homo sapiens]	MHC class I chain-related protein A [Homo sapiens]	[Human gadd45 gene, complete cds.], gene product [Homo sapiens]	_	Homo sapiens clone IMAGE 286356.	VAC protein (AA 1-320) [Homo sapiens]	hypoxia-inducible factor 1 alpha [Homo sapiens]	Gene product with similarity to Rat P8 [Homo sapiens]	RBP-MS/type 1 [Homo sapiens]	KIAA0242 protein [Homo sapiens]	nicotinamide N-methyltransferase [Homo sapiens]	lysyl hydroxylase [Rattus norvegicus]	H.sapiens mRNA for metallothionein isoform 1R.	musculin [Homo sapiens]	cathepsin B [Homo sapiens]	lysyl hydroxylase isoform 2 [Mus musculus]	rtvp-1 [Homo sapiens]	collagen alpha-2(IV) chain [Mus musculus]	•		_	_	G-protein gamma-12 subunit [Homo sapiens]	OASIS protein [Mus musculus]	-	putative tyrosine kinase receptor=UFO [human, NIH3T3, Peptide, 894 aa] [Homo sapiens]	thioredoxin reductase [Homo sapiens]	TX protease precursor [Homo sapiens]	cysteine protease [Homo sapiens]	OB-cadherin-1 [Homo sapiens]			d467L1.2 (vesicle-associated membrane protein 3 (cellubrevin)) [Homo sapiens] CALLA protein (AA 1 - 750) [Homo sapiens]	
	ank Hit E-value	6.00E-88	0	1.00E-139	1.00E-91	0	0	1.00E-178	0	1.00E-18	2.00E-91	0	1.00E-152	0	1.00E-68	4.00E-77	0	0	1.00E-149	0	9.00E-40	0	0	1.00E-105	2.00E-32	1.00E-67	0	0	0	0	0	0	3.00E-86	0	6.00E-39 0	
	GenBank H	g183084	g1405893	g1405893	g403128	g306805	g4063630	g37637	g6636317	g2947054	g1669547	g1663704	g494989	g409059	g1495463	g3599521	g291888	g5852295	g1030053	g1022323	g8101724	g3043597	g219510	g181123	g6563252	g4519621	g55122	g238775	g2832346	g999454	g903934	g1377894	g829623	g8170714	g6580411 g29626	0
	Clone ID	1711206	1854277	1854277	1702350	1418741	2664388	2483173	1711151	3721987	2190284	1940994	604856	1759127	2048551	155904	2806166	1405940	477045	1906574	1906574	2936505	1672442	2054053	1640161	1636639	1358285	1358285	630625	2304121	2304121	434771	450574	1962971	1975129 269456	
	Template ID	230062.4	483043CB1	348205.9	1256295.18	875668CB1	1180189.1	3109992CB1	1250434CB1	1327838.1	2021477CB1	235171.20	149832CB1	1759127CB1	2048551CB1	3282941CB1	2733135CB1	2176269CB1	1218607CB1	1553795CB1	238538.22	246546.9	234223.14	2054053CB1	1613766CB1	233454.3	347699.13	3531583CB1	407096.14	482411.26	482411.25	1258943CB1	1327030.1	025595.22	995174.1 1709732CB1	
0	SEC ED	901	107	108	109	110	111	112	113	114	115	116	117	118	611	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139 140	

Bal DE	6.7	6.7	9.9	6.5	6.5	6.5	6.5	6.4	6.4	6.4	6.4	6.4	6.4	6.3	6.3	6.3	6.2	6.1	6.1	6.1	6.1	6.1	6.1	6.1	9	9	9	9	9	5.9	5.9	5.9	5.8	5.7	
Annotation	SB-2-beta precursor polypeptide (aa -29 to 229) [Homo sapiens]) ZYG homologue [Homo sapiens]	placental protein 5 (PPS) [Homo sapiens]) transfer RNA-Trp synthetase [Homo sapiens]) Human transposon-like element mRNA.	spermidine/spermine N1-acetyltransferase [Homo sapiens]) TRAM protein [Homo sapiens]) CAP, 38 kda intracellular serine proteinase inhibitor [Homo sapiens]	DOC-2 [Homo sapiens]) RNA polymerase II elongation factor ELL2 [Homo sapiens]	DR5 [Homo sapiens]	insulin-like growth factor binding protein 5 (IGFBP5) gene product [Homo sapiens]	eRFI [Homo sapiens]) procollagen alpha 2(V) [Homo sapiens]) collagen type XI alpha-1 isoform A [Homo sapiens]) urokinase receptor-associated protein uPARAP [Homo sapiens]) Wnt-5a [Mus musculus]	_	nonmuscle myosın heavy chain (NMHC) [Homo sapiens]) P63 protein [Homo sapiens]) TRKA [Homo sapiens]) unnamed protein product [Homo sapiens]) platelet-denved growth factor receptor [Homo sapiens]	connexin 43 [Homo sapiens]	MHC-encoded proteasome subunit gene [Homo sapiens]) retinoid X receptor-gamma [Mus musculus]	beta-1,4-galactosyltransferase (AA -77 to 323) [Homo sapiens]	NMB [Homo sapiens]	low-Mr GTP-binding protein Rab32 [Homo sapiens]	. PEA-15 protein [Cricetulus griseus]) cathepsin D [Homo sapiens]	•		putative tyrosine kinase receptor=OFO (numan, intro 1.5, repute, 694 ad [nouno sapiens]
t E-value	1.00E-131	0	1.00E-121	0	0	1.00E-98	0	0	1.00E-140	0	0	1.00E-154	0	0	0	0	0	0	7.00E-11	0	0	0	0	0	0	1.00E-113	0	0	1.00E-55	1.00E-117	9.00E-64	0	0	0	>
GenBank Hit E-value	g36386	g2769562	g484051	g184657	g339899	g338336	g37265	g546088	g1297330	g1946347	g3721878	g505589	g5499721	g2370202	g6165882	g6492130	g202404	g212383	g189036	g297408	g3869113	g7020611	g3478697	g189730	g6563408	g34656	g200882	g29424	g666043	g1388197	g4039117	g179948	g4239883	g517179	g238//2
Clone ID	692827	1865767	2503037	1846209	1997250	063038	1603057	1904994	1976279	1281473	2078364	1686585	1959565	1887959	3598222	2849603	1712327	2056987	2056987	1870941	3176845	3425195	418731	1821971	1997703	2018222	3602501	1736926	1526282	1662688	3215205	3940755	064286	185448	7028747
Template ID	1040610.4	055498.6	181172CB1	2705515CB1	480228.3	360929.39	1989087CB1	995068.16	1217216.1	474426.5	350521.22	1075592.6	1485867CB1	2515360CB1	3290944CB1	441206.15	1712327CB1	1393778CB1	480127.44	1870941CB1	2495110CB1	034711.3	251776.14	239511.5	989878.1	1558664CB1	3602501CB1	5549580CB1	2687977CB1	3168062CB1	245367.2	470587CB1	1631074CB1	347829.12	54 /699 11
SEQ ID NO	141	142	143	1 4	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	191	162	163	164	165	991	191	168	169	170	171	172	173	174	S/1

SEQ ID NO	Template ID	Clone ID	GenBank Hit	E-value	Annotation	Bal DE
176	1251672.1	1453450	g37227	0	tenascin [Homo saprens]	5.6
177	1291022CB1	1291022	g1336027	0	ICE-LAP6 [Homo sapiens]	5.5
178	237405.19	2380381	g602703	1.00E-175	2,4-dienoyl-CoA reductase [Homo sapiens]	5.5
179	2685676CB1	2513883	g517350	0	H.sapiens MT1X gene for metallothionein 1X.	5.5
180	010672CB1	549196	g180130	0	cell adhesion molecule [Homo sapiens]	5.4
181	234630.58	549196	g7705157	0	CD44R4 [Homo sapiens]	5.4
182	332595.5	3249851	g2979420	0	PCDH7 (BH-Pcdh)b [Homo sapiens]	5.4
183	332595.8	3249851	g3513312	0	BH-protocadherin-a [Mus musculus]	5.4
184	335086.1	3602403	g1543068	0	CHASE [Homo sapiens]	5.4
185	1342493CB1	1453748	g6381989	0	adipocyte-denved leucine aminopeptidase [Homo sapiens]	5.4
186	232691.20	2505425	g190877	1.00E-102	ras-lıke protein [Homo sapiens]	5.4
187	238814.2	1417211	g1418782	0	erm [Homo sapiens]	53
188	201571.1	959745	g2072181	0	Rat osteoprotegerin (OPG) protein, complete sequence [Rattus norvegicus]	5.3
189	199882.5	1449824	g2668615	0	similar to drosophila peroxidasin precursor (PID:g531385) [Caenorhabditis elegans]	5.3
190	237487.22	2380042	g791047	2.00E-60	gamma subunit of sodium potassium ATPase like [Homo sapiens]	5.2
161	237487.21	2380042	g791047	3.00E-51	gamma subunit of sodium potassium ATPase like [Homo sapiens]	5.2
192	305557CB1	029564	g2665792	5.00E-91	caveolin-2 [Homo sapiens]	5.2
193	1378745CB1	147184	g162779	0	calpactın I heavy chain (p36) [Bos taurus]	5.2
194	1818836CB1	1818836	g984287	0	NDP52 [Homo sapiens]	5.2
195	137946.3	690994	g7243027	1.00E-168	KIAA1323 protein [Homo sapiens]	5.2
196	2110909CB1	2825369	g165009	0	progesterone-induced protein [Oryctolagus cuniculus]	5.2
197	200578.1	1397926			Incyte Unique	5.2
198	259592CB1	197207	g5911857	1.00E-145	hypothetical protein [Homo sapiens]	5.2
199	5584521CB1	1965863	g219925	1.00E-76	MGC-24 precursor [Homo sapiens]	5.1
200	399428.7	1491445	g3777545	0	nonsyndromic hearing impairment protein [Mus musculus]	5.1
201	117509.4	3012290	g1054903	1.00E-156	gamma-sarcoglycan [Homo sapiens]	5.1
202	3255458CB1	1597330	g2804273	0	alpha actinin 4 [Homo sapiens]	5.1
203	1430889CB1	1856520	g4107433	1.00E-120	hypothetical protein [Homo sapiens]	5
204	445048.6	1856520	g4218185	1.00E-124	hypothetical protein [Homo sapiens]	S
205	4946593CB1	2852818	g337767	0	cerebroside sulfate activator protein [Homo sapiens]	S
206	350605.45	4114209	g453180	0	lamin A [Rattus norvegicus]	S
207	1413644CB1	1413644	g975311	0	adenyl cyclase-associated protein 2 [Rattus norvegicus]	5
208	984009.2	1446475	g1225979	0	H.sapiens mRNA for HMGI-C protein.	4.9
500	627662CB1	1631511	g4102182	0	phosphoenolpyruvate carboxykinase [Mus musculus]	4.9
210	1382932.11	2175008	g1155011	0	nidogen [Homo sapiens]	4.9

Bal DE	4.9	4.9	8.4	4.8	4.8	4.8	4.8 8.4	4.8	4.8	4.8 8.4	4.8	4.8	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.6	4.5	4.5	4.5	4.5	0. 4
Annotation) S100 calcium-binding protein A13 (S100A13) [Homo sapiens]) S100 calcium-binding protein A13 (S100A13) [Homo sapiens]	2 nuclear protein [Homo sapiens]) vimentin [Homo sapiens]) granulin [Homo sapiens]	l vasodilator-stimulated phosphoprotein [Homo sapiens]	tumor suppressing STF cDNA 3 [Homo sapiens]	 brain-derived neurotrophic factor [Homo sapiens] 	7 p35srj [Homo sapiens]	3 p35srj [Homo sapiens]) KIAA0592 protein [Homo sapiens]	2 prefibroblast collagenase inhibitor [Homo sapiens]) protocadhenn [Rattus norvegicus]		•	•	platelet-endothelial tetraspan antigen 3 [Homo sapiens]	j platelet-endothelial tetraspan antigen 3 [Homo sapiens]) calponin [Homo sapiens]	tumor necrosis factor receptor type 1 associated protein [Homo sapiens]	signal transducer and activator of transcription 1; STAT1 [Rattus norvegicus]) alpha1 integrin [Gallus gallus]) hypothetical 19.5 kDa protein [Homo sapiens]	adenylyl cyclase-associated protein [Homo sapiens]) tyrosyl-tRNA synthetase [Homo sapiens]) adipophılın [Bos taurus]) phosphoenolpyruvate carboxykınase [Rattus norvegicus]) phosphoenolpyruvate carboxykınase [Homo sapiens]	•		incyte Unique
Bank Hit E-value	1.00E-86	4.00E-18	0	0	2.00E-40	1.00E-40	1.00E-172	0	0	4.00E-81	6.00E-61	1.00E-134	1.00E-87	2.00E-88	0	1.00E-112	0	0	0	0	1.00E-119	1.00E-125	1.00E-160	1.00E-156	0	0	0	1.00E-125	0	0	0	1.00E-100	0	0	
GenBank Hi	g1542883	g2584789	g183002	g193440	g1694828	g1694828	g793841	g340219	g183613	g1617319	g2655039	g179407	g4193946	g4193946	g3043708	g182483	g4426629	g179095	g6573256	g8248854	g541613	g541613	g1783205	g808915	g6636498	g2582830	g5410274	g178084	g2665519	g5823591	g206067	g307333	g2662375	g1477651	
Clone ID	1624024	2059691	1610993	1610993	2134356	2134356	924319	1522716	812141	1975209	2452650	2488567	2232471	2232471	1457726	591358	1347232	3686211	2204916	548019	2108793	2108793	2696735	1449054	1922533	537580	1830083	030672	1559756	1985104	1975268	1975268	1612306	179929	0/60/97
Template ID	2721850CB1	994902.1	442744.17	442744.21	1908920CB1	399101.31	183198CB1	1397781.7	899496.9	2111330CB1	331591.1	3371198	245011.11	1988468CB1	331470.8	411388CB1	253450.9	351209 16	2124320CB1	903876.1	1238339CB1	245310.36	2696735CB1	338036.2	236484.15	232719.2	462249.1	1187408.1	627856CB1	553078CB1	048612.15	048612.12	1099779.1	1520855CB1	11/9282.1
SEQ ID NO	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	242

Bal DE	4.5	4.5	4.5	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.4	4.3	4.3	4.3		4.3	4.3	4.2	4.2	4.2	4.2	4.2	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.1	4.	4 4	•
Annotation	beta-hexosamındase [Mus musculus]) annexin IV (placental anticoagulant protein II) [Homo sapiens]	steroid sensitive gene-1 protein [Rattus norvegicus]	interferon-gamma [Homo sapiens]	-	_	d136014.2 (collagen, type X, alpha 1) [Homo sapiens]) CG17259 gene product [Drosophila melanogaster]) mannosyl-oligosaccharide 1,3-1,6-alpha-mannosidase [Mus musculus]) glucose-regulated protein [Homo sapiens]	_	Ras negative regulator Rabex-5/Rin2 [Mus musculus]) peptide transporter [Homo sapiens]) peptide transporter [Homo sapiens]) APPH=amyloid precursor protein homolog [human, placenta, Pepude, 763 aa] [Homo sapiens]) follistatin [Bos taurus]	i RER1 protein [Homo sapiens]	helix-loop-helix protein [Homo sapiens]	asparagine synthetase [Homo sapiens]) vinculin [Homo sapiens]) plasma membrane calcium ATPase isoform 1 [Homo sapiens]) FE65-like protein [Homo sapiens]) Shcp52 [Mus musculus]	_) carboxyl termınal LIM domaın protein [Homo sapiens]) calpain II 80 kDa subunit [Rattus norvegicus]	_	i ME491 /CD63 antigen [Homo sapiens]	MHC class II HLA-DQ [Homo sapiens]) MNB [Homo sapiens]) lysyl hydroxylase 3 [Mus musculus]	_	fibulin-2 [Mus musculus]	
E-value	0	1.00E-180	1 00E-126	3.00E-28	1.00E-121	0	4.00E-93	0	0	0	1.00E-114	8.00E-69	0	0	0		0	1.00E-116	2.00E-55	0	0	0	0	0	1.00E-153	0	0	0	1.00E-116	1.00E-137	0	0	0	0 1 00E-120	1.WL-12/
GenBank Hit E-value	g497174	g178699	g7021449	g186513	g186513	g2274966	g7573532	g7295855	g49944	g6900104	g452320	g6822272	g36061	g36061	g300169		g404024	g7688699	g395338	g3341715	g340237	g4165326	g1657752	g558999	g1899055	g1905874	g402666	g36061	g430756	g1791289	g1663726	g5880317	g1235559	g4959705	N71400+8
Clone ID	1658320	030291	544213	2211625	2211625	2814551	2986240	821141	1626460	2884613	1810945	1723035	1634279	1634279	3876715		1577614	2189762	700559	1381654	999864	1724967	2736056	1003486	1003486	2132217	1889060	2668334	2594308	692201	2056290	1901061		1901095	1701071
Template ID	2770449CB1	1430336CB1	903105.6	1327417.14	1327417.10	230712.24	982520.1	311807CB1	1479370CB1	2993696CB1	4004223CB1	453835.19	391741.16	391741.64	1382958.26		232567.4	1720770CB1	253987.19	2047630CB1	238203.11	899410.5	474311.3	2169835CB1	290021.11	267324CB1	2119372CB1	2818482CB1	1330231.11	1330117.5	233402.3	1622313CB1	2939887CB1	1804120CB1	71.005.17
SEQ ID NO	246	247	248	249	250	251	252	253	254	255	256	257	258	259		260	261	262	263	264	265	566	267	268	569	270	271	272	273	274	275	276	277	278	617

SEQ ID						
0N	Template ID	Clone ID	GenBank Hi	Bank Hit E-value	Annotation	Bal DE
280	1285395CB1	015834	g3064263	0	protein 4.1G [Mus musculus]	4
281	036391.3	399035	g37074	1.00E-159	transcription elongation factor [Homo sapiens]	4
282	036391.13	399035	g37074	1.00E-171	transcription elongation factor [Homo sapiens]	4
283	474435.16	1610523	g307155	2.00E-86	MAC30 [Homo sapiens]	4
284	2495292CB1	2495292	g2267585	0	transcription intermediary factor 1 [Homo sapiens]	-4.1
285	251651.4	1645766	g456090	2.00E-76	effector cell protease receptor 1 [Homo sapiens]	-4.2
286	5408483CB1	3493061	g297529	0	NF-M [Mus musculus]	-4.2
287	347876.6	103669	g1184107	0	DNA replication initiator protein [Xenopus laevis]	-4.2
288	1289007CB1	1986737	g6690095	1.00E-145	tetraspanin protein [Homo sapiens]	-4.3
589	233301.18	814216	g180173	0	putative [Homo sapiens]	4.3
290	2157771CB1	2825656	g199023	0	microtubule associated protein 2 [Mus musculus]	-4.3
291	2958028CB1	1569804	g62966	0	NF-E1 [Gallus gallus]	4.4
292	233811.8	1569804	g639594	0	GATA-2 transcription factor {3' flanking region, exon 6}[Homo sapiens].	4.4
293	1270302CB1	1486358	g214862	0	beta-tubulin (Xenopus laevis)	4.4
294	067163CB1	1384823	g29979	4.00E-43	Cks1 protein homologue [Homo sapiens]	4.4
295	002387CB1	2781405	g387005	1.00E-139	proliferating cell nuclear antigen (PCNA) [Homo sapiens]	4.4
396	2798854CB1	4385292	g5262584	0	hypothetical protein [Homo sapiens]	4.4
297	1292280CB1	3496395	g4164381	0	nicotinic acetylcholine receptor alpha-3 subunit [Homo sapiens]	-4.5
298	979248.2	3496395			Incyte Unique	-4.5
299	236240.3	1850531	g4325180	1.00E-109	tetraspan NET-6 [Homo sapiens]	-4.5
300	234427.4	1616315	g1507672	0	GS3955 [Homo sapiens]	-4.6
301	234427.7	1616315	g1507672	9.00E-60	GS3955 [Homo sapiens]	-4.6
302	411205.16	160410	g2865520	0	protein regulating cytokinesis 1 (PRC1) mRNA, complete cds [Homo sapiens]	4.6
303	411205.5	160410	g2865521	0	protein regulating cytokinesis 1; PRCI [Homo sapiens]	-4.6
304	238854.23	1369473	g7707424	1.00E-117	syntaxın 18 [Homo sapiens]	-4.6
305	405008.1	726201	g5926703	4.00E-17	Homo sapiens genomic DNA, chromosome 6p21.3, HLA Class I region, section 15/20.	-4.6
306	372981.9	1576329	g3901272	3.00E-56	ZW10 interactor Zwint [Homo sapiens]	4.7
307	345125.8	180439	g190426	0	protein phosphatase-2A subunit-beta [Homo sapiens]	4.8
308	345125.17	180439	g1777333	3 00E-45	B-regulatory subunit of protein phosphatase 2A [Rattus norvegicus]	4.8
309	1723834CB1	1723834	g434753	0	KIAA0030 [Homo sapiens]	-4.9
310	407588.2		g1035015	1.00E-112	H.sapiens CpG island DNA genomic Msel fragment, clone 71a7, reverse read cpg71a7.rt1a.	ک
311	1970111CB1		g286013	0	KIAA0008 [Homo sapiens]	-5.1
312	058208CB1	467621	g882223	0	triadin [Homo sapiens]	-5.2
313	333461.2	4003342	g559715	0 (KIAA0074 [Homo sapiens]	-5.2
314	002940CB1	161207	g3402293	0	aurora and IPL1-like midbody-associated protein kinase-1 [Homo sapiens]	-5.4

2	Template ID	Clone ID	GenBank Hit	Bank Hit E-value	Annotation	bal DE
315	365153CB1	2375329	g339560	1 00E-178	bone morphogenetic protein 5 [Homo sapiens]	-5.6
316	034181CB1	1316528	g190267	0	poly(ADP-ribose) polymerase [Homo sapiens]	-5.7
317	264633.20	1709017	g4378022	2.00E-84	putative WHSC1 protein [Homo sapiens]	-5.8
318	264633.19	1709017	g6683808	0	MMSET type I [Homo sapiens]	-58
319	1760566CB1	2657680	g1907393	2.00E-79	proneurotensin/proneuromedin N [Homo sapiens]	-5.8
320	3296553CB1	1739904	g609535	0	66 kDa neurofilament protein NF-66 [Mus musculus]	-58
321	199471.2	2414624	g1575534	1.00E-112	Mad2 [Homo sapiens]	-5.8
322	1558165CB1	1403041	g687590	2.00E-36	transmembrane protein [Homo sapiens]	-5.9
323	988665.6	2219234	g2827203	1.00E-114	general transcription factor 2-1 [Homo sapiens]	9-
324	988665.10	2219234	g2827180	4.00E-19	general transcription factor 2-1; alternative splice product [Homo sapiens]	9-
325	334634.1	3230940	g2224577	0	KIAA0318 [Homo sapiens]	9
326	2823239CB1	940823	g207409	0	tyrosine hydroxylase (EC 1 14.16.2) [Rattus norvegicus]	9-
327	021413CB1	1629861	g1488413	1.00E-13	N8 gene product=D52 homolog/leucine zipper protein [Homo sapiens]	-6.1
328	637182CB1	3771476	g293689	0	lamin B [Mus musculus]	-6.1
329	1297347CB1	1813133	g437102	3.00E-88	HMG-1 [Mus musculus]	-6.2
330	149914.15	2446238	g505098	1.00E-113	KIAA0069 [Homo sapiens]	-6.2
331	418689CB1	1646294	g51053	0	GATA-3 factor [Mus musculus]	-6.3
332	2232180CB1	039817	g220136	0	thymidylate synthase [Homo sapiens]	-6.4
333	092267CB1	1932189	g1699046	0	Delta1 [Rattus norvegicus]	-6.9
334	227432.21	617878	g3641300	0	potassium channel [Rattus norvegreus]	-7.1
335	227432.22	617878	g2801452	0	potassium channel; KvEBN1 [Homo sapiens]	-7.1
336	253570.30	1516301	g1778840	0	INS-1 winged helix [Rattus norvegicus]	-7.3
337	253570.32	1516301	g1842255	0	hepatocyte nuclear factor-3/fork head homolog 11B [Homo sapiens]	-7.3
338	3332616CB1	1502188	g1244408	2.00E-17	neuronatin alpha [Homo sapiens]	-7.4
339	1832346CB1	1721744	g339948	0	tropomodulin [Homo sapiens]	7.7-
340	221500.1	1672676	g2130632	0	synaptotagmin XI [Rattus norvegicus]	7.5
341	1794861CB1	1515980	g557272	0	HYL tyrosine kinase [Homo sapiens]	-7.6
342	202239.1	3812392	g200768	0	nbonucleotide reductase subunit M2 [Mus musculus]	-7.6
343	4181211CB1	661492	g1302658	0	neural cell adhesion molecule L1 [Homo sapiens]	-7.7
344	331051.4	661492	g347807	3.00E-96	cell adhesion molecule L1 [Homo sapiens]	7.7-
345	1454418CB1	1525795	g29839	1.00E-172	CDC2 polypeptide (CDC2) (AA 1-297) [Homo sapiens]	7.7-
346	242309.6	1403636	g882147	0	CRMP-62 [Gallus gallus]	-7.8
347	232888.4	129009	g2668414	0	topoisomersae II [Sus scrofa]	8.7-
348	978190.8	3856893	g976235	0	kinesın family protein KIF1a [Mus musculus]	-7.8
240						

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SEQ ID						
0N		Clone ID	Template ID Clone ID GenBank Hit E-value	E-value	Annotation	Bal DE
350	343934.1	1267860	g3641671	0	0 doublecortin [Mus musculus]	-8.3
351	3145862CB1	3176609	g1763259	0	0 collapsin response mediator 1 [Mus musculus]	-8.3
352	1292191CB1	2821341	g5834566	6.00E-65	6.00E-65 chromogranin B (secretogranın 1, SCG1) [Homo sapiens]	-8.3
353	988660.32	1921393	g51442	2.00E-09	putative [Mus musculus]	-9.2
354	2522352CB1	986752	g2506836	0	DNA replication licensing factor MCM7 (CDC47 homolog) [Homo sapiens]	6.6-
355	244622.1	1412749	g4836723	7.00E-90	HMP19 protein [Homo sapiens]	9.01-
356	1555752CB1	3596853	g3192879	0	MAD3-like protein kinase [Homo sapiens]	-10.7
357	2324155CB1	1730052	g292166	1.00E-154	69 kD autoantigen [Homo sapiens]	-11.2
358	1100140.7	2916753	g184236	3.00E-83	high mobility group 2 protein [Homo sapiens]	-13.8
359	1100140.12	2916753	g184236	1.00E-98	high mobility group 2 protein [Homo sapiens]	-13.8
360	3393396CB1	494905	g63099	0	B-myb [Gallus gallus]	-13.8
361	026662.3	485111	g6319178	0	LEK1 [Mus musculus]	-19.2
362	1315515CB1	2821036	g338051	0	secretogranin 11 [Homo sapiens]	-19.4
363	406387.1	2373263	g5689439	1.00E-161	KIAA1051 protein [Homo sapiens]	8.61-
364	1610121CB1	2820985	g181521	0	aromatic amino acid (dopa) decarboxylase [Homo sapiens]	-21.1
365	330839.1 2811651	2811651	g386983	1.00E-164	1.00E-164 N-myc [Homo sapiens]	-37.9

TABLE 2

		IADLL 2		
SEQ ID NO	Template ID	Clone ID	Start	Stop
1	1497123CB1	1497123	300	1261
2	2985802CB1	3553729	6501	7088
3	475532.4	2859033	1	142
4	3138290CB1	1870965	34	5098
5	474310.40	1672744	1418	3957
6	410580.16	1445767	643	2168
7	337518.25	1674454	1234	3035
8	1303785CB1	79576	1100	1335
9	1044033.4	1514989	326	1982
10	1000222.31	690313	969	1529
11	403873.4	2329216	624	1460
12	1383105.12	4049957	136	1158
13	1383354.13	1572533	317	1260
14	697785CB1	2495131	21	332
15	420115CB1	1904751	1420	1958
16	1101453.2	2949427	72	682
17	1399366.20	2055534	4836	5848
18	3072333CB1	1447903	427	2440
19	1270681 1	1804548	1382	2242
20	1505038CB1	1987358	1199	3647
21	1035602.5	1854220	356	804
22	1330167.3	1001730	108	340
23	1003386CB1	1664320	547	1101
24	1097334.1	2483605	132	619
25	959142CB1	2804667	2455	5356
26	1359783CB1	1798209	736	2873
27	063646CB1	557012	544	1852
28	1519595CB1	2056395	938	2657
29	2054176CB1	3142736	660	2545
30	1312325CB1	1319608	2199	2722
31	022404.25	1319608	3805	4401
32	1787335CB1	1958902	726	1992
33	1193648.7	1851696	268	858
34	1193648.1	1851696	6053	6167
35	1867861CB1	1448051	8022	9703
36	5511889CB1	1650238	89	2294
37	3094768CB1	2902903	160	778
38	1256895CB1	1720056	721	2419
39	2019981CB1	1733490	2424	3921
40	2708240CB1	3084122	1730	3549
41	1092427.1	1313183	3747	5208
42	351841.7	1852047	2927	3756
43	022221.43	1314882	8395	10551
44	2190217CB1	78783	207	370
45	410910.3	2518178	2047	4796
46	1966280CB1	1700077	930	1514
47	430669.39	1572555	110	495
48	430669.23	1572555	1213	1596
49	1870753CB1	782235	4047	4691
50	3173735CB1	521139	322	2050
51	1330185.14	2868138	738	1146
52	2314132CB1	3118643	1118	2410
53	2508205CB1	2057296	480	2127
54	3326672CB1	1995380	27	565
55	234202.34	1995380	372	865

TABLE 2

		IADLE Z		
SEQ ID NO	Template ID	Clone ID	Start	Stop
56	078242CB1	1319020	1743	1880
57	220943.20	417451	2272	2861
58	1383320.13	1558081	1275	3419
59	3526170CB1	2242648	533	1276
60	184081.24	27775	188	424
61	1821331CB1	1394401	525	2809
62	3660006CB1	1720114	2517	4383
63	089172.13	3693273	1727	4633
64	3084563CB1	2852042	87	1804
65	241227.17	1402715	515	1496
66	348151.2	1618422	3955	6433
67	1720808CB1	2606307	668	3615
68	998552.6	459651	663	1847
69	040652.35	2508261	541	981
70	040652.36	2508261	2420	2860
71	082155CB1	522294	542	1439
72	190144CB1	1668794	26	812
73	234537.3	1718651	3060	3637
74	1088425.1	162769	25	1178
75	254547.1	3134070	241	1028
76	2676170CB1	3820761	627	1978
77	1092181.1	2105963	37	514
78	471362.33	1720149	443	926
79	471362.27	1720149	319	771
80	1162416.1	2102320	1	157
81	252151.12	1599344	1054	1635
82	252151.7	1599344	1	579
83	358892.1	2057260	3649	3810
84	1296867CB1	3506985	209	793
85	337518.7	3506985	285	2721
86	1344279CB1	2771046	1591	3649
87	2731776CB1	2057601	1553	2381
88	1090035.1	1994472	40	450
89	1089929.9	2683564	646	778
90	2723092CB1	2633207	793	1058
91	2174489CB1	2173208	2599	3196
92	1253978CB1	1867652	606	2740
93	2274011CB1	1909488	606	1154
94	3119737CB1	2733928	183	414
95	1384695.102	1514318	2903	3243
96	257332CB1	1402228	1435	3048
97	2972880CB1	1636171	1163	1832
98	550425CB1	550425	482	1771
99	014284CB1	1822716	696	1862
100	1091854.7	1708528	4484	8482
101	138709.5	2844989	793	2272
102	375954.1	1404153	1066	3654
103	1262781CB1	3511216	947	1540
104	282761.16	3511216	2458	2924
105	3090708CB1	1283532	849	1996
106	230062.4	1711206	4892	6599
107	483043CB1	1854277	294	756
108	348205.9	1854277	564	977
109	1256295.18	1702350	828	1323
110	875668CB1	1418741	302	747

TABLE 2

TABLE 2					
SEQ ID NO	Template ID	Clone ID	Start	Stop	
111	1180189.1	2664388	425	958	
112	3109992CB1	2483173	5	1537	
113	1250434CB1	1711151	2302	2787	
114	1327838.1	3721987	39	327	
115	2021477CB1	2190284	139	873	
116	235171.20	1940994	3600	3851	
117	149832CB1	604856	466	1002	
118	1759127CB1	1759127	2503	3425	
119	2048551CB1	2048551	1	558	
120	3282941CB1	155904	993	1501	
121	2733135CB1	2806166	523	1903	
122	2176269CB1	1405940	790	2462	
123	1218607CB1	477045	300	889	
124	1553795CB1	1906574	2283	2722	
125	238538.22	1906574	1044	1569	
126	246546.9	2936505	358	860	
127	234223.14	1672442	4807	6314	
128	2054053CB1	2054053	332	869	
129	1613766CB1	1640161	1176	1567	
130	233454.3	1636639	930	1580	
131	347699.13	1358285	2709	3065	
132	3531583CB1	1358285	2458	3191	
133	407096.14	630625	2268	3868	
134	482411.26	2304121	29	519	
135	482411.25	2304121	1168	1318	
136	1258943CB1	434771	1739	3350	
137	1327030.1	450574	353	1225	
138	025595.22	1962971	4003	5656	
139	995174.1	1975129	568	2327	
140	1709732CB1	269456	1219	3491	
141	1040610.4	692827	557	1390	
142	055498.6	1865767	3980	4262	
143	181172CB1	2503037	8	1168	
144	2705515CB1	1846209	677	2204	
145	480228.3	1997250	555	1014	
146	360929.39	63038	85	296	
147	1989087CB1	1603057	651	1324	
148	995068.16	1904994	462	925	
149	1217216.1	1976279	12140	12702	
150	474426.5	1281473	306	1426	
151	350521.22	2078364	1076	1891	
152	1075592.6	1686585	3257	4529	
153	1485867CB1	1959565	1635	2290	
154	2515360CB1	1887959	4110	4667	
155	3290944CB1	3598222	2388	3877	
156	441206.15	2849603	967	2806	
157	1712327CB1	1712327	1675	2673 5780	
158	1393778CB1	2056987	5339 1037	5789 1246	
159	480127.44	2056987	686	2204	
160 161	1870941CB1 2495110CB1	1870941 3176845	568	815	
162	034711.3	3425195	2588	3084	
163	251776.14	418731	2388	3391	
164	239511.5	1821971	3967	5570	
165	989878.1	1997703	2259	3042	
105	707070.1	1771103	2237	3042	

TABLE 2

		TABLE 2		
SEQ ID NO	Template ID	Clone ID	Start	Stop
166	1558664CB1	2018222	354	799
167	3602501CB1	3602501	1141	1784
168	5549580CB1	1736926	1057	2249
169	2687977CB1	1526282	23	2808
170	3168062CB1	1662688	520	1064
171	245367.2	3215205	452	2440
172	470587CB1	3940755	1735	2236
173	1631074CB1	64286	1477	1652
174	347829.12	185448	492	2202
175	347699.11	2058242	3889	4665
176	1251672.1	1453450	6281	7539
177	1291022CB1	1291022	1115	2019
178	237405.19	2380381	273	1420
179	2685676CB1	2513883	465	882
180	010672CB1	549196	119	635
181	234630.58	549196	213	788
182	332595 5	3249851	160	733
183	332595.8	3249851	4129	4680
184	335086.1	3602403	3018	3387
185	1342493CB1	1453748	1684	2248
186	232691.20	2505425	554	1692
187	238814.2	1417211	1660	4002
188	201571.1	959745	278	1827
189	199882.5	1449824	4198	5529
190	237487.22	2380042	250	443
191	237487.21	2380042	595	756
192	305557CB1	29564	55	257
193	1378745CB1	147184	979	1422
194	1818836CB1	1818836	34	2284
195	137946 3	690994	5224	6258
196	2110909CB1	2825369	938	2140
197	200578.1	1397926	1163	2312
198	259592CB1	197207	443	751
199	5584521CB1	1965863	131	653
200	399428.7	1491445	1662	2204
201	117509 4	3012290	72	1586
202	3255458CB1	1597330	123	615
203	1430889CB1	1856520	236	669
204	445048 6	1856520	497	923
205	4946593CB1	2852818	1624	2578
206	350605.45	4114209	1448	1913
207	1413644CB1	1413644	782	2021
208	984009 2	1446475	68	808
209	627662CB1	1631511	1128	2113
210	1382932.11	2175008	4209	4703
211	2721850CB1	1624024	1162	2690
212	994902.1	2059691	530	1222
213	442744.17	1610993	1331	1866
214	442744.21	1610993	1571	2138
215	1908920CB1	2134356	755	1192
216	399101.31	2134356	514	1144
217	183198CB1	924319	774	1255
218	1397781.7	1522716	1328	1966
219	899496.9	812141	1463	2552
220	2111330CB1	1975209	1034	1781

TABLE 2

		IADLE 2		
SEQ ID NO	Template ID	Clone ID	Start	Stop
221	331591.1	2452650	50	429
222	337119.8	2488567	742	1319
223	245011.11	2232471	879	1228
224	1988468CB1	2232471	886	1876
225	331470.8	1457726	3107	3620
226	411388CB1	591358	486	842
227	253450.9	1347232	12543	14884
228	351209.16	3686211	1030	2447
229	2124320CB1	2204916	3	2226
230	903876.1	548019	2801	5026
231	1238339CB1	2108793	179	677
232	245310.36	2108793	900	1367
233	2696735CB1	2696735	72	1519
234	338036.2	1449054	661	1416
235	236484.15	1922533	3229	4192
236	232719.2	537580	2541	3462
237	462249.1	1830083	2469	3616
238	1187408.1	30672	1252	1462
239	627856CB1	1559756	311	829
240	553078CB1	1985104	731	1832
241	048612.15	1975268	2605	2853
242	048612.13	1975268	1114	1662
243	1099779.1	1612306	1043	1732
244	1520855CB1	179929	4384	6269
245	1179282.1	2870970	730	1328
243 246	2770449CB1	1658320	843	1776
246 247	1430336CB1	30291	650	805
248		544213	4275	4675
	903105.6	2211625	4273	435
249	1327417.14		4 0 5	995
250	1327417.10	2211625 2814551	40 3	940
251	230712.24	2986240	18	3113
252	982520.1	821141	641	1853
253	311807CB1	1626460	2350	3565
254	1479370CB1		13	2488
255	2993696CB1	2884613	425	955
256	4004223CB1	1810945 1723035	4103	5200
257	453835.19	1634279	1823	2346
258	391741.16	1634279	2996	3441
259 260	391741.64 1382958 26	3876715	591	902
261	232567.4	1577614	511	1140
			323	811
262	1720770CB1	2189762	493	1406
263	253987.19	700559	815	1897
264	2047630CB1	1381654	4229	5092
265	238203.11	999864	4019	4432
266	899410.5	1724967		
267	4743113	2736056	3931	6660
268	2169835CB1	1003486	1792	2109
269	290021.11	1003486	2586	3038
270	267324CB1	2132217	1179	1454
271	2119372CB1	1889060	1770	3137
272	2818482CB1	2668334	404	1219
273	1330231.11	2594308	333	1159
274	1330117.5	692201	649	1299
275	233402.3	2056290	5739	6369

TABLE 2

		TABLE 2		
SEQ ID NO	Template ID	Clone ID	Start	Stop
276	1622313CB1	1901061	1640	2538
277	2939887CB1	1375115	2059	2667
278	1804120CB1	1901095	2380	2963
279	245485.12	1901095	630	1083
280	1285395CB1	15834	1238	1533
281	036391.3	399035	1109	1635
282	036391.13	399035	2283	2683
283	474435.16	1610523	1326	2035
284	2495292CB1	2495292	1974	3637
285	251651.4	1645766	881	1434
286	5408483CB1	3493061	489	3217
287	347876.6	103669	290	2962
288	1289007CB1	1986737	942	1758
289	233301.18	814216	2032	2585
290	2157771CB1	2825656	5088	5612
291	2958028CB1	1569804	1259	1854
292	233811.8	1569804	316	734
293	1270302CB1	1486358	1376	2197
294	067163CB1	1384823	66	639
295	002387CB1	2781405	884	1288
296	2798854CB1	4385292	1174	3091
297	1292280CB1	3496395	1271	1842
298	979248.2	3496395	1	192
299	236240.3	1850531	472	1929
300	234427.4	1616315	911	1423
301	234427.7	1616315	1	625
302	411205 16	160410	195	679
303	411205.5	160410	1903	3093
304	238854.23	1369473	913	1296
305	405008.1	726201	69	488
306	372981.9	1576329	62	417
307	345125.8	180439	552	1110
308	345125.17	180439	270	840
309	1723834CB1	1723834	2901	3240
310	407588.2	1640108	1458	1771
311	1970111CB1	1970111	1059	2805
312	058208CB1	467621	609 1538	1459
313 314	333461.2	4003342	86	2064 1222
315	002940CB1 365153CB1	161207 2375329	509	1794
316	034181CB1	1316528	1946	3633
317	264633.20	1709017	1940	562
318	264633.19	1709017	2523	3069
319	1760566CB1	2657680	536	798
320	3296553CB1	1739904	2395	2868
321	199471.2	2414624	125	1463
322	1558165CB1	1403041	431	1842
323	988665.6	2219234	878	1327
324	988665.10	2219234	276	797
325	334634.1	3230940	3713	5552
326	2823239CB1	940823	1174	1778
327	021413CB1	1629861	210	1669
328	637182CB1	3771476	1110	1582
329	1297347CB1	1813133	275	1067
330	149914.15	2446238	412	2382
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TABLE 2

		IADLE Z		
SEQ ID NO	Template ID	Clone ID	Start	Stop
331	418689CB1	1646294	1618	2260
332	2232180CB1	39817	798	963
333	092267CB1	1932189	805	1262
334	227432.21	617878	447	1001
335	227432.22	617878	843	1376
336	253570 30	1516301	2588	3043
337	253570.32	1516301	2747	3519
338	3332616CB1	1502188	15	547
339	1832346CB1	1721744	1109	2734
340	221500.1	1672676	3901	5215
341	1794861CB1	1515980	779	1949
342	202239.1	3812392	0	1680
343	4181211CB1	661492	2001	2372
344	3310514	661492	1175	1676
345	1454418CB1	1525795	336	1776
346	242309.6	1403636	3247	3729
347	232888 4	129009	3843	5647
348	978190.8	3856893	10	991
349	2700132CB1	2470485	412	985
350	343934.1	1267860	8048	9390
351	3145862CB1	3176609	1646	2820
352	1292191CB1	2821341	9	2541
353	988660 32	1921393	284	703
354	2522352CB1	986752	443	2551
355	244622.1	1412749	1845	2383
356	1555752CB1	3596853	27	3642
357	2324155CB1	1730052	112	1683
358	1100140.7	2916753	1	542
359	1100140.12	2916753	575	1152
360	3393396CB1	494905	166	2601
361	026662.3	485111	7806	10241
362	1315515CB1	2821036	31	2342
363	406387.1	2373263	5566	6690
364	1610121CB1	2820985	517	1895
365	330839.1	2811651	1054	2499